RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/573,999_

Source: _1FWP_

Date Processed by STIC: _4/13/06_

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IFWP

RAW SEQUENCE LISTING   DATE: 04/13/2006
PATENT APPLICATION: US/10/573,999   TIME: 10:01:02

Input Set : **A:\BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25.txt**
Output Set: **N:\CRF4\04132006\J573999.raw**

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      3 <110> APPLICANT: Bayer CropScience GmbH
      5 <120> TITLE OF INVENTION: Plants with increased activity of a Class 3 branching enzyme
      7 <130> FILE REFERENCE: BCS 03-5005-PCT
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/573,999
C-->  9 <141> CURRENT FILING DATE: 2006-03-30
      9 <150> PRIOR APPLICATION NUMBER: EP 03090324.9
     10 <151> PRIOR FILING DATE: 2003-09-30
     12 <160> NUMBER OF SEQ ID NOS: 6
     14 <170> SOFTWARE: PatentIn version 3.1
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 1004
     18 <212> TYPE: DNA
     19 <213> ORGANISM: Solanum tuberosum
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     26 caagatgatc agattaatta catctacaat tggtggtcat gcatacctca acttcatggg     180
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     30 ttcactggct aaccgtcgct gggatctatt ggaagatgtt gtacattatc aattgttctc     300
     32 atttgataag ggtatgatgg acttggataa aaatgggaga attttgtcca gaggtcttgc     360
     34 caacattcac catgtcaatg atactaccat ggtgatttct tacttgagag gtcccaatct     420
     36 ctttgtgttc aactttcatc ctgtcaattc atatgaaaga tacattatag gtgtggaaga     480
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     40 acttggccat gatcagaata ttcaaagaac cattagtaga agagctgatg gaatgagatt     600
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     44 aagagcatga tcactctagt aatcaaagtg cctcatatga tgacacaaaa ggaaaggttc     720
     46 tacattgccc ttacactgat caatattgac acctttccga ggtgagtttc tgtgattctt     780
     48 gagcagactg ttggctagtc aattatcatg aacttttgcc ttcagcatcc ggatagtcgc     840
     50 ttctcctgtg caatgagggc atggacgaat ttttttttgg cttgtcatgg gggtcataag     900
     52 catccgccag attaagattt cacaggcctc gagtaaaacc atcacttact ttaaggatac     960
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     59 <212> TYPE: DNA
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     67 ccgggctcga gtttcgaggt gtagatgctc agcaacggag caaccgccac cgcaacgacg     180
     69 gaagcaacga ccggagaagt acaaacagtc ggaggaaggg aaaggaatcg atcctgttgg     240
     71 atttctcagc aaatacggca ttactcataa agcgtttgct caatttcttc gtgaaagata     300
     73 taaatcattg aaggacttga aggatgaaat attgactcgt catttcagtc tcaaggagat     360
     75 gtctactggg tatgaattaa tgggtatgca tcgcaacata caacatcgag tggatttctt     420
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 83 caattatgcg gaggactatg gtaaaggtga cacgggtatt accgtcgagg aaatctttaa    660
 85 aaaagcaaat gatgagtatt gggaacctgg agaagatcgc ttcattaaat cacgttatga    720
 87 ggtggcagca aagttatatg aggaaatgtt cggaccaaat ggacctcaaa cagaagagga    780
 89 actagaagca atgcctgatg cagctacacg atacaaaact tggaaagagc aacaaaaaga    840
 91 ggatccggca agcaatttgc catcgtatga tgtggtagat agtggaaaag aatatgatat    900
 93 ttacaatatt ataggtgatc ctgaatcgtt taagaaattt cgtatgaaac agcctcctat    960
 95 tgcttactgg ttagaaacta aaaagggaag gaaaggctgg ttacagaaat atatgcctgc   1020
 97 tttacctcat ggaagcaaat acagggtgta ttttaacaca ccaaatgggc ctcttgaacg   1080
 99 agttcctgcg tgggccaatt ttgtcattcc agatgcaggc gggatggcat tagcagtcca   1140
101 ttgggaacca cctcctgaat atgcttataa atggaaacac aagctaccag tcaagcctaa   1200
103 gtccttgcgc atatatgaat gtcatgttgg catctctggc caggaaccaa aagtttcatc   1260
105 tttcaatgat tttattagca aggtccttcc gcatgtaaaa gaagctggat acaatgcaat   1320
107 acaaattatt ggagttgttg agcacaagga ttatttcact gttggatata gagtgaccaa   1380
109 ttttttatgct gttagtagcc gttatggcac accggatgac ttcaagcgct tggttgatga   1440
111 agcacatggg cttggactgc ttgtcttttt ggagattgtg cactcttatg cagcagcaga   1500
113 tgaaatggtt gggttatctc tttttgatgg agcaaatgat tgctatttcc acactggtaa   1560
115 acgtggacac cacaaattct ggggcacacg gatgttcaaa tatggagatc ttgatgttct   1620
117 gcactttctt ctttcaaatc tgaactggtg ggtggaggag tatcatgtcg atggcttcca   1680
119 ttttcattcg ctctcgtcca tgttgtatac gcataatgga tttgcttcat ttactggtga   1740
121 catggatgaa tactgtaacc aatatgttga caaggaggcc ttattgtacc tcatattagc   1800
123 aaatgaagta ttacatgctc ttcatcctaa tgtgatcacg attgctgagg atgcaactct   1860
125 gtatcctgga ctctgcgatc caacatctca aggtggactg ggctttgatt attttgccaa   1920
127 tctttctgcc tcagagatgt ggcttgcatt acttgaaaat actcctgatc atgaatggtg   1980
129 catgagtaag attgttagca cattagtggg cgatagacaa aatactgata aaatgctttt   2040
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134 <210> SEQ ID NO: 3
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136 <212> TYPE: DNA
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139 <220> FEATURE:
140 <221> NAME/KEY: CDS
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148 cgccagtgtg atggatatct gcagaattcg cttaaca atg ctc tct ctg tcg gat    116
149                                             Met Leu Ser Leu Ser Asp
150                                              1               5
152 tca att cga att tct tca cca ttg agc gat tct cgt ctt agt ttt cta    164
153 Ser Ile Arg Ile Ser Ser Pro Leu Ser Asp Ser Arg Leu Ser Phe Leu
154          10              15              20
156 tct caa acc gga agc aga acc agt cgc cag ctt aaa ttt gtt cgc agc    212
157 Ser Gln Thr Gly Ser Arg Thr Ser Arg Gln Leu Lys Phe Val Arg Ser
158          25              30              35
160 cgc cgg gct cga gtt tcg agg tgt aga tgc tca gca acg gag caa ccg    260
161 Arg Arg Ala Arg Val Ser Arg Cys Arg Cys Ser Ala Thr Glu Gln Pro
162          40              45              50
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164 cca ccg caa cga cgg aag caa cga ccg gag aag tac aaa cag tcg gag    308
165 Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu Lys Tyr Lys Gln Ser Glu
166 55              60              65                    70
168 gaa gag aaa gga atc gat cct gtt gga ttt ctc agc aaa tac ggc att    356
169 Glu Glu Lys Gly Ile Asp Pro Val Gly Phe Leu Ser Lys Tyr Gly Ile
170              75              80                    85
172 act cat aaa gcg ttt gct caa ttt ctt cgt gaa aga tat aaa tca ttg    404
173 Thr His Lys Ala Phe Ala Gln Phe Leu Arg Glu Arg Tyr Lys Ser Leu
174              90              95                    100
176 aag gac ttg aag gat gaa ata ttg act cgt cat ttc agt ctc aag gag    452
177 Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg His Phe Ser Leu Lys Glu
178              105             110                   115
180 atg tct act ggg tat gaa tta atg ggt atg cat cgc aac ata caa cat    500
181 Met Ser Thr Gly Tyr Glu Leu Met Gly Met His Arg Asn Ile Gln His
182              120             125                   130
184 cga gtg gat ttc ttg gaa tgg gct cca ggt gct cgc tac tgt gct ctg    548
185 Arg Val Asp Phe Leu Glu Trp Ala Pro Gly Ala Arg Tyr Cys Ala Leu
186 135             140             145                   150
188 att ggt gac ttc aat ggg tgg tca aca act ggt aac tgt gcc aga gag    596
189 Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr Gly Asn Cys Ala Arg Glu
190              155             160                   165
192 ggt cat ttt ggt cat gac gat tat ggg tat tgg ttt att att ctt gaa    644
193 Gly His Phe Gly His Asp Asp Tyr Gly Tyr Trp Phe Ile Ile Leu Glu
194              170             175                   180
196 gat aaa tta cgt gaa gga gaa gaa cct gat aaa ttg tat ttt caa cag    692
197 Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp Lys Leu Tyr Phe Gln Gln
198              185             190                   195
200 tac aat tat gcg gag gac tat gat aaa ggt gac acg ggt att acc gtc    740
201 Tyr Asn Tyr Ala Glu Asp Tyr Asp Lys Gly Asp Thr Gly Ile Thr Val
202 200             205             210
204 gag gaa atc ttt aaa aaa gca aat gat gag tat tgg gaa cct gga gaa    788
205 Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu Tyr Trp Glu Pro Gly Glu
206 215             220             225                   230
208 gat cgc ttc att aaa tca cgt tat gag gtg gca gca aag tta tat gag    836
209 Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val Ala Ala Lys Leu Tyr Glu
210              235             240                   245
212 gaa atg ttc gga cca aat gga cct caa aca gaa gag gaa cta gaa gca    884
213 Glu Met Phe Gly Pro Asn Gly Pro Gln Thr Glu Glu Glu Leu Glu Ala
214              250             255                   260
216 atg cct gat gca gct aca cga tac aaa act tgg aaa gag caa caa aaa    932
217 Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr Trp Lys Glu Gln Gln Lys
218              265             270                   275
220 aag gat ccg gca agc aat ttg cca tcg tat gat gtg gta gat agt gga    980
221 Lys Asp Pro Ala Ser Asn Leu Pro Ser Tyr Asp Val Val Asp Ser Gly
222 280             285             290
224 aaa gaa tat gat att tac aat att ata ggt gat cct gaa tcg ttt aag    1028
225 Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly Asp Pro Glu Ser Phe Lys
226 295             300             305                   310
228 aaa ttt cgt atg aaa cag cct cct att gct tac tgg tta gaa act aaa    1076
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232 aag gga agg aaa ggc tgg tta cag aaa tat atg cct gct tta cct cat   1124
233 Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr Met Pro Ala Leu Pro His
234               330             .335            340
236 gga agc aaa cac agg gtg tat ttt aac aca cca aat ggg cct ctt gaa   1172
237 Gly Ser Lys His Arg Val Tyr Phe Asn Thr Pro Asn Gly Pro Leu Glu
238               345             350             355
240 cga gtt cct gcg tgg gcc aat ttt gtc att cca gat gca gac ggg atg   1220
241 Arg Val Pro Ala Trp Ala Asn Phe Val Ile Pro Asp Ala Asp Gly Met
242       360             365             370
244 gca tta gca gtc cat tgg gaa cca cct cct gaa tat gct tat aaa tgg   1268
245 Ala Leu Ala Val His Trp Glu Pro Pro Pro Glu Tyr Ala Tyr Lys Trp
246 375             380             385             390
248 aaa cac aag cta cca gtc aag cct aag tcc ttg cgc ata tat gaa tgt   1316
249 Lys His Lys Leu Pro Val Lys Pro Lys Ser Leu Arg Ile Tyr Glu Cys
250               395             400             405
252 cat gtt ggc atc tct ggc cag gaa cca aaa gtt tca tct ttc aat gat   1364
253 His Val Gly Ile Ser Gly Gln Glu Pro Lys Val Ser Ser Phe Asn Asp
254               410             415             420
256 ttt att agc aag gtc ctt ccg cat gta aaa gaa gct gga tac aat gca   1412
257 Phe Ile Ser Lys Val Leu Pro His Val Lys Glu Ala Gly Tyr Asn Ala
258               425             430             435
260 acg caa att att gga gtt gtt gag cac aag gat tat ttc act gtt gga   1460
261 Thr Gln Ile Ile Gly Val Val Glu His Lys Asp Tyr Phe Thr Val Gly
262       440             445             450
264 tat aga gtg acc aat ttt tat gct gtt agt agc cgt tat ggc aca ccg   1508
265 Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser Ser Arg Tyr Gly Thr Pro
266 455             460             465             470
268 gat gac ttc aag cgc ttg gtt gat gaa gca cat ggg ctt gga ctg ctt   1556
269 Asp Asp Phe Lys Arg Leu Val Asp Glu Ala His Gly Leu Gly Leu Leu
270               475             480             485
272 gtc ttt ttg gag att gtg cac tcc tat gca gca gca gat gaa atg gtt   1604
273 Val Phe Leu Glu Ile Val His Ser Tyr Ala Ala Ala Asp Glu Met Val
274               490             495             500
276 ggg tta tct ctt ttt gat gga gca aat gat tgc tat ttc cac act ggt   1652
277 Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp Cys Tyr Phe His Thr Gly
278               505             510             515
280 aaa cgt gga cac cac aaa ttc tgg ggc aca cgg atg ttc aaa tat gga   1700
281 Lys Arg Gly His His Lys Phe Trp Gly Thr Arg Met Phe Lys Tyr Gly
282       520             525             530
284 gat cct gat gtt ctg cac ttt ctt ctt tca aat ctg aac tgg tgg gtg   1748
285 Asp Pro Asp Val Leu His Phe Leu Leu Ser Asn Leu Asn Trp Trp Val
286 535             540             545             550
288 gag gag tat cat gtc gat ggc ttc cat ttt cat tcg ctc tcg tcc atg   1796
289 Glu Glu Tyr His Val Asp Gly Phe His Phe His Ser Leu Ser Ser Met
290               555             560             565
292 ttg tat acg cat aat gga ttt gct tca ttt act ggt gac atg gat gaa   1844
293 Leu Tyr Thr His Asn Gly Phe Ala Ser Phe Thr Gly Asp Met Asp Glu
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294          570              575              580
296 tac tgt aac caa tat gtt gac aag gag gcc tta ttg tac ctc ata tta   1892
297 Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala Leu Leu Tyr Leu Ile Leu
298          585              590              595
300 gca aat gaa gta tta cat gct ctt cat cct aat gtg atc acg att gct   1940
301 Ala Asn Glu Val Leu His Ala Leu His Pro Asn Val Ile Thr Ile Ala
302      600              605              610
304 gtg gat gca act ctg tat cct gga ctc tgc gat cca aca tct caa ggt   1988
305 Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys Asp Pro Thr Ser Gln Gly
306 615              620              625              630
308 gga ctg ggc ttt gat tat ttt gcc aat ctt tct gcc tca gag atg tgg   2036
309 Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu Ser Ala Ser Glu Met Trp
310              635              640              645
312 ctt gca tta ctt gaa aat act cct gat cat gaa tgg tgc atg agt aag   2084
313 Leu Ala Leu Leu Glu Asn Thr Pro Asp His Glu Trp Cys Met Ser Lys
314          650              655              660
316 att gtt agc aca tta gtg ggc gat aga caa aat act gat aaa atg ctt   2132
317 Ile Val Ser Thr Leu Val Gly Asp Arg Gln Asn Thr Asp Lys Met Leu
318          665              670              675
320 ttg tat gca gaa aat cac aac cag tcc att tct gga ggt cgt tcc ttc   2180
321 Leu Tyr Ala Glu Asn His Asn Gln Ser Ile Ser Gly Gly Arg Ser Phe
322      680              685              690
324 gca gaa ata ctg att ggt aac tcc ttg ggg aaa tct tcc ata tca caa   2228
325 Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly Lys Ser Ser Ile Ser Gln
326 695              700              705              710
328 gag tca tta ctt aga ggc tgc tcg tta cac aag atg atc aga tta att   2276
329 Glu Ser Leu Leu Arg Gly Cys Ser Leu His Lys Met Ile Arg Leu Ile
330              715              720              725
332 aca tct aca att ggt ggt cat gca tac ctc aac ttc atg ggc aat gaa   2324
333 Thr Ser Thr Ile Gly Gly His Ala Tyr Leu Asn Phe Met Gly Asn Glu
334          730              735              740
336 ttt ggt cac cca aag aga gta gag ttt cca atg tca agc aac aat ttc   2372
337 Phe Gly His Pro Lys Arg Val Glu Phe Pro Met Ser Ser Asn Asn Phe
338          745              750              755
340 tcc ttt tca ctg gct aac cgt cgc tgg gat cta ttg gaa gat gtt gta   2420
341 Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp Leu Leu Glu Asp Val Val
342      760              765              770
344 cat tat caa tta ttc tca ttt gat aag gat atg atg gac ttg gat aaa   2468
345 His Tyr Gln Leu Phe Ser Phe Asp Lys Asp Met Met Asp Leu Asp Lys
346 775              780              785              790
348 aat ggg aga att ttg tcc aga ggt ctt gcc aac att cac cat gtc aat   2516
349 Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala Asn Ile His His Val Asn
350              795              800              805
352 gat act acc atg gtg att tct tac ttg aga ggt ccc aat ctc ttt gtg   2564
353 Asp Thr Thr Met Val Ile Ser Tyr Leu Arg Gly Pro Asn Leu Phe Val
354          810              815              820
356 ttc aac ttt cat cct gtc aat tca tat gaa aga tac att ata ggt gtg   2612
357 Phe Asn Phe His Pro Val Asn Ser Tyr Glu Arg Tyr Ile Ile Gly Val
358          825              830              835
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VERIFICATION SUMMARY   DATE: 04/13/2006
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date